

AMENDMENT

Please amend the application, without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents.

IN THE CLAIMS

1. (Previously Presented) A reverse genetics system for screening and identifying antinflaviviral compounds.
2. (Canceled)
3. (Currently Amended) The reverse genetics system according to ~~claims 1 and 2~~ claim 1 comprising a full-length lineage I WNV cDNA clone.
4. (Currently Amended) The reverse genetics system according to ~~claims 1 and 2~~ claim 1 comprising a lineage I WNV replicon.
5. (Previously Presented) The reverse genetics system of claim 3, wherein the full-length lineage I WNV cDNA comprises a promoter sequence operably linked to the WNV cDNA and a first nucleotide sequence encoding a first reporter.
6. (Previously Presented) The reverse genetics system of claim 4, wherein the lineage I WNV replicon comprises a promoter sequence operably linked to the WNV replicon and a first nucleotide sequence encoding a first reporter.
7. (Currently Amended) The reverse genetics system of any one of claims 5 ~~and~~ or 6, wherein the first nucleotide sequence encoding a reporter is selected from the group consisting of a nucleotide sequence encoding a luciferase reporter, a green fluorescent protein reporter, beta-galactosidase, an oxidase, a peptidase, a glycosidase, a phosphatase, a fluorescent protein reporter, and an antibiotic resistance marker.
8. (Previously Presented) The reverse genetics system of claim 5, wherein the WNV cDNA further comprises a second nucleotide sequence encoding a second reporter.
9. (Previously Presented) The reverse genetics system of claim 6, wherein the WNV replicon further comprises a second nucleotide sequence encoding a second reporter.
10. (Currently Amended) The reverse genetics systems of any one of claims 8 ~~and~~ or 9, wherein the second reporter is a selectable marker.
11. (Previously Presented) The reverse genetics systems of claim 10, wherein the selectable marker is neomycin-resistance marker (Neo).

12. (Currently Amended) The reverse genetics systems of any one of claims 6 ~~and~~ or 9, wherein the first nucleotide sequence encoding the first reporter is a nucleotide sequence encoding green fluorescent protein and the second nucleotide sequence encoding the second reporter is a neomycin resistance marker.
13. (Currently Amended) The reverse genetics system of any one of claims 5 ~~and~~ or 6, wherein the promoter is selected from the group consisting of a prokaryotic promoter, a eukaryotic promoter, and a viral promoter.
14. (Previously Presented) The reverse genetics system of claim 13, wherein the viral promoter is selected from the group consisting of SP6, T7, and T3.
15. (Currently Amended) The reverse genetics system of any one of claims 5 ~~and~~ or 6, wherein the nucleotide sequence encoding a reporter further comprises an internal ribosome entry site (IRES) to control translation of said reporter.
16. (Previously Presented) A recombinant plasmid comprising the reverse genetics system of claim 5.
17. (Previously Presented) A recombinant plasmid comprising the reverse genetics system of claim 6.
18. (Canceled)
19. (Canceled)
20. (Previously Presented) A cell line stably replicating the reverse genetics system of claim 11.
21. (Previously Presented) A cell line stably replicating the reverse genetics system of claim 12.
22. (Canceled)
23. (Canceled)
24. (Canceled)
25. (Canceled)
26. (Canceled)
27. (Canceled)
28. (Previously Presented) The reverse genetics system of claim 8, wherein the first nucleotide sequence encoding a reporter and second nucleotide sequence encoding a reporter are joined in the same reading frame and are together preceded by an IRES, wherein said IRES directs the translation of the first and second reporters.

29. (Previously Presented) The reverse system of claim 9, wherein the first nucleotide sequence encoding a reporter and second nucleotide sequence encoding a reporter are translationally fused and are preceded by an IRES, wherein said IRES directs the translation of the first and second reporters.
30. (Currently Amended) The reverse genetics systems of any one of claims 28 ~~and~~ or 29, wherein the first nucleotide sequence encoding a reporter and second nucleotide sequence encoding a reporter are linked by an autoprotease nucleotide sequence.
31. (Previously Presented) The reverse genetics systems of claim 30, wherein the autoprotease nucleotide sequence is a foot and mouth disease virus 2a autoprotease nucleotide sequence.
32. (Previously Presented) A recombinant plasmid containing a cDNA sequence corresponding to WNV lineage I, wherein said recombinant plasmid further comprises a promoter sequence adapted to control cDNA transcription and at least one nucleotide sequence encoding a reporter, wherein said reporter indicates the level of transcription of said cDNA sequence corresponding to WNV lineage I.
33. (Canceled)
34. (Canceled)
35. (Canceled)
36. (Canceled)
37. (Canceled)
38. (Canceled)
39. (Canceled)
40. (Canceled)
41. (Canceled)
42. (Canceled)
43. (Canceled)
44. (Canceled)
45. (Previously Presented) A DNA molecule comprising a DNA sequence encoding a mRNA of a lineage I WNV genome, said DNA sequence having a 5' and a 3' end, said DNA molecule adapted to report the transcription of said DNA sequence, said DNA molecule comprising:

(a) a deletion in said DNA sequence corresponding to one or more structural genes of said lineage I WNV genome;

(b) a promoter at said 5' end of said DNA sequence;

(c) a nucleotide sequence encoding a reporter at said 3' end of the DNA sequence;

wherein said promoter is operably linked and adapted to control the transcription of said DNA sequence and said nucleotide sequence encoding said reporter.

46. (Previously Presented) The DNA molecule according to claim 45, wherein said lineage I WNV genome is according to SEQ ID NO.2.

47. (Previously Presented) The DNA molecule according to claim 45, wherein said reporter is selected from the group consisting of luciferase, green fluorescent protein, beta-galactosidase, oxidase, peptidase, glycosidase, phosphatase, a fluorescent protein, and an antibiotic resistance marker.

48. (Previously Presented) The DNA molecule according to claim 45, where said reporter is green fluorescent protein.

49. (Previously Presented) The DNA molecule according to claim 45, wherein said reporter is luciferase.

50. (Previously Presented) The DNA molecule according to claim 45, wherein said one or more structural genes is selected from the group consisting of the capsid, envelope, and membrane genes.

51. (Previously Presented) The DNA molecule according to claim 45, wherein said deletion is in the capsid, envelope, and membrane genes of said lineage I WNV genome.

52. (Previously Presented) The DNA molecule according to claim 45, wherein said reporter is a selectable marker.

53. (Previously Presented) The DNA molecule according to claim 52, wherein said selectable marker is a neomycin resistance marker (Neo).

54. (Previously Presented) The DNA molecule according to claim 45, wherein said promoter is selected from the group consisting of SP6, T7, and T3.

55. (Previously Presented) The DNA molecule according to claim 45, wherein said DNA molecule contains a second nucleotide sequence encoding a reporter, wherein transcription of said second nucleotide sequence encoding said second reporter under control of said promoter.

56. (Previously Presented) The DNA molecule according to claim 55, wherein the second reporter is selected from the group consisting of luciferase, green fluorescent protein, beta-galactosidase, oxidase, peptidase, glycosidase, phosphatase, a fluorescent protein, and an antibiotic resistance marker.

57. (Previously Presented) The DNA molecule according to claims 55, wherein the first and second nucleotide sequences encoding first and second reporters are optionally preceded by an internal ribosome entry site (IRES), wherein said IRES facilitates translation of said first and second reporters.

58. (Previously Presented) The DNA molecule according to claim 45, wherein the DNA sequence is a lineage I WNV replicon and said reporter is GFP or luciferase.

59. (Previously Presented) A DNA molecule comprising a DNA sequence encoding a full-length and fully-infectious mRNA of a lineage I WNV genome, said DNA sequence having a 5' and a 3' end, said DNA molecule adapted to report the transcription of said DNA sequence, said DNA molecule comprising:

- (a) a promoter at said 5' end of said DNA sequence;
- (b) a first nucleotide sequence encoding a first reporter gene at said 3' end of the DNA sequence;

wherein said promoter is adapted to control the transcription of said DNA sequence and said reporter gene.

60. (Previously Presented) The DNA molecule according to claim 59, wherein said lineage I WNV genome is according to SEQ ID NO.2.

61. (Previously Presented) The DNA molecule according to claim 59, wherein said reporter is selected from the group consisting of luciferase, green fluorescent protein, beta-galactosidase, oxidase, peptidase, glycosidase, phosphatase, a fluorescent protein, and an antibiotic resistance marker.

62. (Previously Presented) The DNA molecule according to claim 59, where said first reporter is green fluorescent protein.

63. (Previously Presented) The DNA molecule according to claim 59, wherein said first reporter gene is luciferase.

64. (Previously Presented) The DNA molecule according to claim 59, wherein said first reporter is a selectable marker.

65. (Previously Presented) The DNA molecule according to claim 64, wherein said selectable marker is a neomycin resistance marker (Neo).
66. (Previously Presented) The DNA molecule according to claim 59, wherein said promoter is selected from the group consisting of SP6, T7, and T3.
67. (Previously Presented) The DNA molecule according to claim 59, wherein said DNA molecule comprises a second nucleotide sequence encoding a second reporter, wherein the transcription of said second nucleotide sequence encoding the second reporter is under control of said promoter.
68. (Previously Presented) The DNA molecule according to claim 67, wherein the second reporter is selected from the group consisting of luciferase, green fluorescent protein, beta-galactosidase, oxidase, peptidase, glycosidase, phosphatase, a fluorescent protein, and an antibiotic resistance marker.
69. (Previously Presented) The DNA molecule according to claims 68, wherein the first and second nucleotide sequences encoding said first and second reporters are optionally preceded by an internal ribosome entry site (IRES), wherein said IRES facilitates translation of said first and second reporters.
70. (Canceled)
71. (Canceled)
72. (Canceled)
73. (Canceled)
74. (Canceled)
75. (Canceled)
76. (Canceled)
77. (Canceled)
78. (Canceled)
79. (Canceled) The method according to claim 78, wherein said method further comprises the step of providing access to the database to a third party, wherein said third party analyzes the database to identify the flavivirus inhibitor.
80. (Canceled)
81. (Canceled)
82. (Canceled)

- 83. (Canceled)
- 84. (Canceled)
- 85. (Canceled)
- 86. (Canceled)
- 87. (Canceled)
- 88. (Canceled)
- 89. (Canceled)
- 90. (Canceled)
- 91. (Canceled)
- 92. (Canceled)
- 93. (Previously Presented) A cell line comprising the DNA molecule according to claim 45.
- 94. (Canceled)
- 95. (New) The reverse genetics system of claim 3, wherein the full-length lineage I WNV cDNA clone is according to SEQ ID NO:1 or SEQ ID NO:2.
- 96. (New) The reverse genetics system of claim 3, wherein the full-length lineage I WNV cDNA clone is according to SEQ ID NO:2.